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OM Of: 88-99-525-998A-1 t. A_G-6-5-11101.*
                                                                                                                                                                                                                                                              Copyright (c) 1993-2000 Compugen Ltd.
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IVI (366(VV, )Herseneb/Lessanst/U.ept=5/781);
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(8 H882/graduta/genesed/genesedp/AAT994
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28.1 Supposation processing generally, AAP and AAAP 1. A Second to the control of the control of
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and betwoestures therapeutic agent.
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Fullio, 5.466
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- 101 TAGGGACAGGGAGAGAGAGATAGTGTGTGTGCAAGGAAAATATATG 150
- 151 CACCCTCAAAATAATTCGATTTGCTGCAAAGTGCCACAAAGGAAGCTA 200
- 201 CTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGACTGCAGGGAGT 250 67 ILCULYTASHASPCYSPLOGIYPTGGIYGINASPThrAspCysArgGluC
- 251 GYGAGAGGGGTGCYTCACCCYTCAGAAAACCACCYCAGACACTGCCYC 300
- 301 AGCIGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGACTCTTCTTG 350 101
  - 351 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 400
- 401
- ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
- 451 AATGGGAGCGTGCACCTCTCCTGCCAGGAGAACAGGAGAACACCGTGTGCAC 500
  - 501 CTGCCATGCAGGTITCTTICIAAGAAAAAGAGAGTGIGICCCGGTAGTA 550
- ACTGTAAGAAAAGCCTGGAATTGCACGAACTTGTGAATAAGAAATTGAG 600 551
- 201 AsnVallysGlyThrGluAspScrGlyThrThTTHTHTHTHTHTHTT
- 651 CATTITCITIGGECTITGCCTTTTATCCCTCCTCTTCATTAATGT 200
- 701 AFGGGTANGAAGGGGGGAAGTCPAAGGFGTACFCGATTGTTTGTGGGAAA 750
- 8.00
- 801 GGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGG 850 284 267 aAlaBroAshProSciPhaScrProThiProGlyPhethiProThiLenG
- 284 lyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 851 GOTTICAG RECOGNICOCCAG FIRMACETICAGETICAGETICACETATACE
- 951 CTATCAGGGGCTGACCCCATCCTTGCGACACGCCTCGCGACCCCA 1000

1001		1050
35		350
1051	CTAGACACTGATGACCCGCGACGCTGTACGCCGTGGTGSAGAACGTGC	1100
3.0		367
1101	CCCGTTGCGCTGGAAGGAATTCGTGCGGGCGCCTAGGGCGCACGACG	1150
36	367 oProLeuArqTrpLysGluPheValArqArqLeuSlyLeuSerAspHisG	384
1151	AGATCGATCGCTGGACTGCAGACGGCCCTGCCTGCGCGAA	1200
38	384 lulleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln	400
1201	TACAGCATGCTGGCGACCTGGAGGCGGCACGCACGCGCGCG	1250
40		417
1251	GCIGGAGCIGCIGGAAGGGIGCIGGGGGAAAAGGIGCIGGGGGGGG	1300
41		434
1301	TGGAGGACATCGAGGGGGCTTTGCGGCCCGGCGGCCCTCCCGGCCGCG	1350
£.		450
1351	51 CCCAGTCTCTCAGA 1365	
451		

seq\_name: /SIDS2/qcqda!a/ueneseq/qeneseqp;\AA199} DAT-AAR42059

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AAK42059 standard, Protein; 455 AA
                                                                                                        (first entry)
                                                                                                                                              Lambda derived TNF-R.
seq_documentation_block:
                                                                                                      29-APR 1994
                                                              AAR12059;
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Human; tummour necrosis factor receptor; FNF-R; interleukin-1 receptor; IL-1R; lusion protein; linker; TNF: IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis, septic shock; pulmonary fibrosis; silicosis; allogialt; xenograft; rejection; graft verses host discase, sepsis; inflammation; allergy;

/note- "Signal peptide" /note- "Mature hTNF-R" Location/Qualifiers 41..455 autoimmune dysfunction. Lambda-91.10-7clu1bp. Homo sapiens Peptide Protein 

92US-0860710. 93W0 US02938 (IMMV ) IMMUNEX CORP 26 MAR 1993; 30-MAR-1992;

14-OCT-1993. WO9319777-A

W. L. 1993 336592,42. N-PSDB; AAQ49932.

Smith CA;

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fartor receptor (INF'R) and the sequences in AAR4200 61 represent human interleukin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                    The sequences given in AAR42058-59 repressent human tumour necrosis
New Tusion protein tumour necrosis factor and human interleukin-1
                                  receptor - iseful in therapy, diagnosis and assays of e.g. Theumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNF-R-linker-TNF-R-Linker-IL 1R
IL-1R-linker-TNF-R-linker-TNF-R or
INF-R-linker-TNF-R
                                                                                                                                                                                Disclosure, Page 57-59, 85pp, English.
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The linker many comparisons of 100 amino acids selected from 619, Asp, Ser. The and Ala. These linkers separate the individual mocifies by such a distance that each component of the insimportion is capable of folding into the secondary or tertiary structure required to its biological activity. These fusion proteins may be used in therapy, disposals and assays for conditions incidated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, careford malaria, allogated and achieves multiple secterosis, pulmonary ilbrossis and salicosis, cerebral malaria, allogated shock, inflammation, allorates and autoimmune dysfunctions.

Sequence 455 AA;

Porcent (dentity: 100.000 Percent Similarity: 100.000 Quality: 2487.00 5.466 Ratio: aliqnment\_scores: aliqument\_block:

Align seg 1/1 to: AAK42059 from: 1 to: 455

US-09-525-998A-1 x AAR42059

- 1 MetGlyLeuSerThrValProAspLeuLeuLeuLeuValLeuLeuGl 17 1 ATGGGCCICTCCACCGIGCCIGACTGCIGCIGCCACIGGIGCTCCTGGA 50
- 51 CCTCTTGGTGGGAATATAPPRETEAGGGGTTATTGGACTGGTGCCTCACC 100
- 101 TAGGGACAGGGAGAGAGAGAGATAGTGTGTGCCCAAGGAAAATATATC 150 14 euglyAspargGlüfysargAspScrValCysfroGlüGfylystyrfle 50
- 151 CACCCTCAAAATAATICGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
- 67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGLuC 84
- 251 GIGAGAGGGGCICCIICACCACIICAGAAAACCACICAGACACIGGCIC 300 84
- AGCIGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTG 350 HITTH HITTH HITTH HITTH HITTH HITTH HITTH HITTH HITTH SerCysSerLyscysArallysol MetGlyClsValsLulleserSerCy 117
- 35] GAGACIGGACCGGGACGIGIGIGGCIGGGAGGAAGAAGAAGAGAGGAGGG 400

	3.4	ALIMITATEMENT IN THE STANDARD	47 -
	45:	AATGGGACGTG SACCETTETT OCCAGRACAARACAAA NAGGGGAAT TITTITITI OTTETTITITITITITITITITITITITITITITITITIT	5ge 16.7
	50.i	CONTAIN AND INTERPRESENTATION OF STATEMENT O	J. X.
	17 TH	ACIGITAMAMANA (GRASI-SCACGAM-HAGGATTACTO - AGAILGAG [[H] [] H H H H H H H H H H H H H H H H	6000 2000
	65.1 201	AATSTTAAGSTSTASTGAGGAGGAGGAGGAGGGGGGGGGG	65u 217
	651 217	CATHTOLLIGGIZTINGCHINATOPICATOLLICATISSHITAAIGI HIHHIII AAHHITTIHHHIIIIHHHIIIAHAA MICPheiberskeigi eegystealeasen tentoupheile Typteumeti	700
	701	ATGGTACTAAGGGTGGAAGGGCAAGGTCTATGCATTGTTGTGGGAAA 	750
	751 251	ICGACAPTICAAAAAGAGGGGGGGGGGGGAGAAGAATAATAAGAGAATAAGAGAGGGGGG	60.0
	801 267	GGCCCCAAAM MAGALLIAGLOCCACLMAGGLLCAM MAGALAMAGCLGCALLIA ALLIA LILLIA LILLIA LILLIA LILLIA ALAMAGAAMAGAAMAGAAMAGAAMAGALAMAGAAAMAGAAAMAGAAMAGAAMAGAAMAGAAAMAGAAMAGAAMAGAAAMAGAAAMAGAAMAGAAAMAGAAAMAGAAAMAGAAAMAGAAAMAGAAAMAGAAAMAGAAAMAGAAAA	850 284
	851 284	GCTICARICCGGGCCCAAITCCACAITCACCTCGAACTCCAACIATAAC 	100
	901 301	GOOGLIACHGEGCAANHIGGGGCHOODGAGAGAGAANOACCAO THEELE FEELEN HILLE GELLA HELLE GAACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	950
	951 317	CTAICASSOGGEGGACCTIGGGAGGGGGGGGGGGGGATTTTTTTTTTTTTTT	1000 334
	434	ICCCCAAD CONTICAGAAGIGGAAGAA GAAGAC CAGAAGACAAGAAGAA HILLIHHILL GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	1650 450
-	351	CTAGAPACTGAFCACCCCCGGAGGGGAAAAGGGGGGGGGGGGGGGG	1100
-	181 367	CCCCTIONAL SAABAATIONA SANGA, ABANCO, AS SANCACA HTTLE HTTLE HTTLE HTTLE HTTLE TO THE CONTROL OF TABLET TO OPTOLOGA POTELY SCHOPLEVALATION AND SACRASPHISS	1150
-	151	AGATYOATPOSYTOSAGOOGGGAAAASPOGATGYCTAA SYAASAGAAA [TITLETITES TROUGHED STEELETITET TO SEE TAATAA STEELET [STEENSPACTION OF TASKO SYAGOTS TO AGATE.	1266
	201 401	TACAOTA IOCUGA, MATUROAGIO BACO CARO CARO CARONICA PER	1250
	25.1	GC190A P. P. P. GGCACOCTOTO P. A. 190A P. P. P. 1913 P.	_ 4
1	301	TGGAGGACATCGAGGAGATATITG, GEORGESCOORD LE CEGUCACE	1 45.03

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This sequence represents human p55 tumout merrosis factor (INF-R). Expression of this receptor is requiated by shedding of the extractional releptor from the February February of the shed in respects to dilletent inducing agents, e.g. phorhol myristate accepter (PMA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AAR75012) in the
                                                                                                                                                                                                                                                                                                                                                                    p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "minor C terminus for soluble p55 TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protease capable of eleaving soluble tumbur mecrosis factor (TNF) receptor - trom cell-bound TNF receptor, useful for aniagonising deleterious effects of TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "major C terminus for soluble p55 TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                        epidermal growth factor receptor; EGF-R; profease; inhibitor; phorbol myristate acetate; PMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "peptide used in creation of chimeras"
Seq_name: 78:10827geggafa7genesegzgenesegp/AA1995_0aft-AAP75694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "essential for shedding reaction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N terminus of soluble p55 TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212..234
/note- "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "qlycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "qlycosylation site"
193..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "spacer region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loration/Qualifiers
                                                                                                                                                                                  seq_documentation_block.
ID AAR75084 standard; Protein; 455 AA.
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                                                                                                  451 ProSerteuLeuArg 455
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                                                                                                                                                                                                                                                                                                                         p55 TNF-R.
                                                                                                                                                                                                                                            AAR75084;
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receptor (EGF-R) that are represented by AAR75007-11. This spacer region was subjected to deciction mutations (AAR75018-25) and substitutions (AAR75026-47). Of the spacer region, the most important tosidous are Asm 172, Val 173, Lys 174 and 91; 175 with Val 173 Luis the land most important to these. The shedding of the receptor is independent of the side chain identity of these residues with the exception of a limited dependence on the identity of Val 173. Mutations which alter the
          This region is located close to a site of cleavage
                                                                                                                                                                                                                                                                                                                                                        conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-K Iragments of these inhibitors can be seen in AAR75017-9, AAR75025, AAR7503-3, and AAR75042-3. These protease inhibitors can be used for enhancing TNF function.
extracellular domain—This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 INF-R and murine epidermal growth lactor.
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seq\_documentation\_block:

Percent Identity: 180.000

Percent Similarity: 100.000

L-141112: 2487.00

d. Tgnment\_scores:

5.455

H44.100

Site.

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This invention describes novel homogeneous insoluble proteins (1), their (10) soluble itraneous (1), their (10) soluble itraneous in the invention have anti-inflammatory and antimalatia activity. (1) and (ia) are used (i) extra diseases in Which INF is involved (v.g. septimators block, autoimmune glowernlonephylis, corebral malaria, immune its prosess and inflammation). (ii) to purity INF (iii) to identify INF (ant) avoinsts and (iv) for diagnosists of the instance of INF in Foly Nichas, Antibedies tailed and instance in the internation of the internation of
                                                                                                                                                                                                        Tailout nectosis tactor binding protein; INF) insoluble protein; agonist;
                                                                                                                                                                                                                                anti inflammatory, antimalarial, freatment, septic shock: inflammation, autoimmune glomeratonephritis, cerebral malaria, immune glomeratonephritis, cerebral malaria, immune response:
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/lahel- siqual_peptide
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AAY30934 standard; Protein; 455 AA.
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                                                                                                    5661-124-81
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                                                   4AY 309 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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alignment_block:
US U9-525-998A-1 x AAY30934
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Aliqu seq 1/1 to: AAY 80934 trom: 1 to: 455

- 1 ATGGGCCTCTCCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 50
- 51 GCTGTTGGTGGGGAATAIACCTTTAAGGGIIALLGGAACIGGTGCTCACC 100
  - 101 TAGOGGACAGGGAGAAGAGATAGTGTGTGTCCCAAGGAAAATATATC 150
- 151 CACCCTCAAAATAATTGGATTTGGTGTACCAAGTGGCACAAAGGAAGCTA 200 51 HisProGlaAsnAsnScriteCysCysThrtySCysHistySClyThrty 67
- 201 CITGIACAAIGACIGICCAGGGGGGGGAGAAGAAIACGGACIGCAGGGAGT 250
- 300 251 GTGAGAGGGGCTGCTTCAGGGTTTCAGAAAAGCAGGTGAGAGACTGGCCTC 67 rLeufyrAsnAspCysProClyProClyClnAspThrAspCysArgGluC
- 35Û 301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTTG 101 SerCysSerLysCysArgLysCluMetGlyGlnValGlufleSerSerCy
- 400 351 CACAGTGGACCGGGACACGGTGTGTGGCTGCAGGAAGAAACCAGTACCGGC
  - 401 ATTALTIGAGIGAAAACTTTTCCAGIGCTTCAATTGCAGCCTCTGCCTC 450
- 134
- 500

451 ProSerLeuLeuArg 455

- 550 501 CIGCCATGCAGGTTTCTTAAGAGAAAAGGAATGTGTCTCTGTAGTA
  - 551 ACTGTAAGAAAACCCTGGAGTGCAAGTTGTGCCTAACTTGAG 600
- - 60] AATGITAAGGGGAGTGAGGACTCAGGGACCACAGTGCTGTTGCCCCTGGT 650
- CATITICITIGGEORI GOCFILIA FOCE CONTINUE PARTICAL DA PARTICITA PART 217 IllePhePheGlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetT 234
- 701 ATCGCTA-CARCASTOCAABTCCAARTCTATTCCATTGTT CATGGAAA 750 HTHTHTHTHTHTHTHTHTH
  - 234 yrArqTyrGlcArqTrpLysSerLysLeuTyrSerTleValCysGlyCys 250 751 TCGACACPIGAAAAAAAAGGGGGGGGGAAGGAACTAACTACTAATTAAGCCCTT ROO

(YUGG/) YU G.

284		300
301	Programmer of proceday in the Geograph Standard Geograph of the Commission of the Co	950
951	CTATCAGGGGGTGACCCCATCCTTGCGAACAGCCCTGCGACCCCATCCTTTTTTTT	1000 334
1001 334	TYPPECAAPQECETTTGAGAAGTGGGAGGAGGAGAAAAGCCAAAAGAGGTTTTTTTT	1050 350
1051 351	CTAGACAPTGA CACCOCAGACAPTGTACGCGTGGTGGTGGAGGAGGTGCC 	1100 367
1101 367	COUNTIBUNCTERNAGEATTERIGGEROCUMBERTGARGEROCACG	1150 384
1151 384	AGATOGATOGACOGAGAAGGGGGGGGGGGGGGGGGGGAAA 	1200
1201	TAPAGPATGCTGRAPGACCTGRAPGCGGCCACACGCGGGGGGGGGGCGCCCCCCCCCCCC	1250
1251	GCTGGAGTTGTTGTGATGTGTGCTGGGACATGGACTGCTGGGGCGCCTTTTTTTT	1300 434
1301	TGGAGGACATCTAGGAGGTTTTGCGGGGGGGGGGGGGGG	1350
1351	CCCAGICTICACAA 1365	

Human, Jeath domain containing receptor; DR3-VI; cancer; autoimmune disorder; inflammation; cardiovascular disorder; infection; seq\_name: /SIDS2/grada/a/geneseq/geneseqp/AA20000 DAT AAR46266 Human tumour necrosis factor receptor 1. neurodegenerative disease; angiogenesis. AAB36266 standard, Protein; 455 AA (HUMA-) HUMAN GENOME SCI INC 99US-0136741. 21-APP-2009; 2000W0-USI0741 94US-0130488 20-FEB 2001 (linst entry) (UNMI ) UNIV MICHIGAN. seq\_documentation\_block W0200064465-A1 22-APF-1999; 28-MAY - 1999; Homo sapiens 02-NCV-2000. AAB36266; 

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The present invention provides the protein and coding sequences for two death domain containing receptors, designated DR3 and DR3-VI. These receptors are involved in apoptosis, and the sequences given can be used in the treatment of cancers, infectious, cardiovascular disorders such as arrhythmias, ischacmia, ancurysms, arrental prolusive diseases, owherlisms and congenital heart defects, neurodegenerative diseases including Alzheimer's and Parkinson's diseases, autoimmune diseases including sciencesis, arthritis, diabetes, Graves' disease, asthma and psociasis, and to promote and wound healthy.
                                                                                                                                                                                      Treating graft versus host disease, cancer, immunodeliciency or an autoimmune disease comprising administering an antibody to Death Domain Containing Receptor proteins and a second therapeutic agent -
                                                                                                         Dillon PJ, Dixit VM;
                                                                                                                                                                                                                                                                       Disclosure, Fig 3; 273pp; English.
                                                                                                         Ni J, Gentz RL.
(NEUJZ) NE J.
(GENTZ) CENTS E D.
(DILLZZ) DILLON P J.
                                                                                                                                              WPI; 2000 687263/67
                                                           (DIXIA) DIXIT V M
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## Sequence 455 AA;

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Gaps: 0 Persont Identity: 100 000
                                                                                                                                    Align seg 1/1 to: AAB36266 from: 1 to: 455
                               5.466
160 040
            Ouality: 2487_00
                                                                                                 US-09-525-998A-1 x AAB36266
                                 Ratio:
                                            Percent Similarity:
alignment_scores:
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- 1 ATGGGCCICTCCACCIGGCIGACTGCTGCTGCTGCTGCTGCTGGA 50 1 Met.GlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
- 51 GCIGTTGGTGGGAAIAIAPPCCCICAGGGGTTATTGGACTGGIGCCTCACC 100

- 201 CITGIACAATGACIGITGTAGGCCGGGGAGGATAGGGACTGCAGGAGT 250 67 riesTyrAspAspCycProSlyFrcSlySlpAspThrAspCysArgGluC 84
- 251 GIGAGAGGGGCIGCIIGAAAGGIAAAACCACCCCAGACAGGGCCIC
- 801 AGCIGCICCAAAIGCCGAAAAGAAATGGGTCAGGIGGAGAICTCIIG 350 101 SerCysSerLysCysArgLysSlaMetSlySlnValSlulleserSerCy 117
- 351 CACAGIGGACCCGGACACGIGIGIGIGGCIGCAGGAAGAAGCAGIACCGGC 400
- 401 ATTATEGRAGEGAAAACCTTTICCAGFGCTTCAAITGCAGCCICIGCCTC 450

1100 1301 IGGAGGACAICGAGGAGAGAGGIIIIGUGGGCCCGGCGGCCTTCCCGCCGCGCC 1350 1101 CCCCTTCACATGGAACCAATTGGTGCCCCCATAGGGCTGAGCGACCACA 1150 1151 AGAICGAICGGGGGGGGGGGGGGGGGGGGGGGGGGGGAA 1200 1201 TACACCATICCTGORGAMITTGCAGGMCGMCMMMMMCGGGGGATT250 , , L., 801 GOCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCAGGCTGAGCCTGG 850 300 317 olyrGlnGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProl 334 401 TyrSerMetLeuAlaThrTrpArqArqArqThrProArqArqGluAlaTh 417 | HELFILLIE | FEFT | HELFILLE | H 501 CIGCCATGCACCTTCTTCTAAGAAAAAGGAGTGTCTCTGTAGTA 601 AATGITAAQGGCACTGAGGACTCAGGGAGTAGAGTGCLATTGCGCCTGGT 650 001 Acavallysed yThrdlaAcpSerdlyThrThryalle.Lc.frcLe.Va 277 701 AIGGGIAGGAAAGIGGAAAGIGGAAGGIGIAGGCATIGTTGIGGGAAA 750 551 ACTGTAAGAAAAGCCTGGAGTGCACGAAGIIGIGGCIACCCAGAIIGAG 65] CATLING LIGGLOFI GOCTTI LA ROCCIOTETTOATEGOTI LAATEN 217 Tillelike i hediguveligsbendanskar beutaurihan ada guadMatt 751 ICGACACCITAAAAAGAGGGGACTIGAAGGAAGIACTACTAACAACCC 284 TypheScribtoValProSerSerThrPheThrSerSerThrTyrThr 901 CCCCCTARTILICACAACTITGCCGCTAGCCAGAGAGAGAGGIGGCACTAC 1051 CTAGACACTGALGACCCGGGGGGGGGGCCGGGGGGGGGAGAAGGTGGC 351 LeuAspInrAspAspProAlaThrLeuTyrAlaValValTinAsnValPr 851 GTICAGICGGIGGGAAHGCAGHGAAGIGAAGIGAAGHGAAHAIAIA 1001 ICCCCANTOCCCTTCAGAAGIGGGAGACAGAGTCCAAAAGAAAAAAA 

1 ATGGGCC1C1CCACCG1GCC1GACCTGC1GCTGCCACTGC1GCTGGA

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The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or letracycline of the compounds for treating and/or prevoiting acute inflammatory responses and discases. Such diseases include acute inflammatory conditions associated with viral haemorrhagic diseases (including diseases caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplanted bone marrow-induced graft-versus-host disease, soptic shock, immune complex-induced colitis, rerebrespinal fluid inflammation, multiple selecosis, inflammatory responses associated with trauma, systemic inflammatory response syntrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver latture, inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p75 receptor; antilullammatory; haemostatic; antibacterial, sepsis; immunosuppressive; immunomodulator; cardiant; cytostatic; cachoxia; neuroprotective; respiratory; inflammatory; information; (tolin's disease; maltiple solutosis, autolamnus diseated, cardiovascular diseated; chronic myeloqenous leakaemia, inflammator; howel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bunyaviridea, Filoviiidae, Flaviviridae or Archaviridae viruses),
parasitic diseases, bacterial intections, sepsis, cachexia, autoimmue
disorders, acute cardiovascular events, chionic myelogenous leukaemia a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Lumour necrosis factor; TNF: INF-alpha; INF-beta; p55 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel compositions comprising tetracycline or tetracycline-like compounds for the treatment and/or presention of acute inflammatory responses and diseases, e.g. septic shock and immune complex-induced
                                                                                                                                                                  remediate tensore the AALCOC TAL AARCON O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour necrosis factor p55 receptor
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                                                                                                                                                                                                                                                                                              AAB37800 standard; Protein; 455 AA
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1351 GGCAGICTICICAGA 1365
                                                                                   451 ProSerLeuLeuArg 455
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                                                                                                                                                                                                                                                          seq documentation_block:
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Developed 1 departity: 100,000 Gaps:

Ratio: 5.466 Percent Similarity: 100 000

Quality: 2487.00

aliqument\_scores:

Align seq 1/1 to: AAB 37800 from: 1 to: 455

US-09-525 998A-1 x AAB37800

aliqument\_block

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301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGAICTCTTCTTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 CACAGIGGAPTGGGGAAPTGTGTGGC113CAGGAAGAAGCAGIACCGGC 400
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                                                                                                                                                                                                                                                                               ISI CACCCICAAAATAATTCGATTTGCTGTACCAAAGTGCCACAAAGGAAGCIA 200
                                                                                                                                                                                                                                                                                                                                                                                  201 CITGIACAALGACCIGCAGGCGGGGCAGGATAGGGACTGCAGGGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 GIGAGAGGGGTGJICACGGJICAGAAAAAGAGGCAGAGAGAGIGGGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SerCysSerLysCysArgLysGluMetGlyGluValGluIleSerSerCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 sThi Val AspargaspThi Val CysGiyGysArgiysAsuGiniyr ArgH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGGCTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AsnGlyThrValHisLeuSerCysGluGluLysGluAsnThrValCysTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 CIGCCAIGCAGHITCIIICIAAGAGAAAACGAGIGIGICICCIGIAGIA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCAGATTGAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 AATGTTAAGGGGAGTGAGGAGTGAGGAGAGAGTGGTGTTGGCGGTGGT 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 [1] cPhePhedlyJeuCysLeuLouSerLeafeuPhelleGlyLeaMetT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      701 AICGCTACCAACGGIGGAAGICCAAGCTCIACTCCAIIGITIGIGGGAAA 750
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                                                                                                                                                                                                      51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysClyThily 67
                                                                                                                                                                                                                                                                                                                                                                                                                                  67 rieuryrAsnAspCysProClyProClyClnAspChrAspCysArgCluC 84
                                                                                                   101 IAGGGGACAGGAGAGAGAGAGATAGIGIGIGGCCCCCAAGGAAAAIAIAIC
651 CATTICITIBGIOLPIGCOTITIALCOCPONICATORITIGATIAATGE
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Human; TNFE; turmour necrosis factor; TEG receptor; immunosuppressive; antiallergic; a
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                                                                                                                                                                                                                                                                    951 CTATCACACACATGACCATATTICITICASACACACACACACACACACA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 lufleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
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                                                                                          301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317
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The present sequence is INFR L, a member of the tumour necrosis factor deceptor lamily A novel human tumour necrosis and or receptor lamily. A novel human tumour necrosis and or receptor lamily. A novel human tumour necrosis also known as beating and the properties also known as beating the neceptor 6. 189 polypeptides, polynucleotides or validation of itenting, preventing or disquessing continuous and animono partiable immunodeficiency, x-1 intend appropriate the second continuous continuous disabilities, allergic enceptacions, and thinkis allergic enceptacions, epilepsy, cancer, disabelles and astimate, miv intentions epilepsy, cancer, cardiovascular diseases and other neurotopical diseases.
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1001 PECCEAACCECTICAGAAGFGGGACACACCCCACACACCCACACACC 1050
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                                              551 ACTGTAAGAAAAGCCFGGAGTGCACGAAGFFGTGGCCFACCCCAGAFFGAG 600
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                                                                                                                                                                                651 CATITICITIGGICILIGGCILLIAICCCICCICCICAIGGLILAAGGE 200
                                                                                                                                                                                                                                                 751 TOBACACTGAAAAAGAGGGGGGGGGGGTTGAAGGAACTACTACTAAGCCCCT 800
                                                                                                                                                                                                                                                                                                                                                                              851 GCTTCAGICCCGTGCCCAGITCCACCTTCACCICCAGCTCCACCIATACC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 ProdlyAspCysProAsmPhcAlaAlaProArgArgCluValAlaProPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 oTyrGlnGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProl 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 rLendluLeulLeuglyArqVallenArqAspNetAspLeuLeudluCysL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AsnGlyThrValHisteuSerCysGlnGluLysGlnAsnThrValCysTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                              367 oProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 lulleAspArqLeuGluLeuGlnAsnGlyArqCysLeuArqGluAlaGln 400
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Polynuclectides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor i (TNFK1), useful for studying the blological function of TNFR1 and identifying drugs targeting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNPR) gaps. The present sequence is the TNPR protein. The sequence of the whole gene is given in AAA95102, AAA495103 and AAA4404. The polymorphisms were identified by amplifying and AAA4404. The polymorphisms were identified by amplifying and sequencing regions of the gene. Tweive polymorphisms are acuse a charge in the TNPR protein. The TNPR polymorphisms may be useful for studying the biological function of TNPR as well as for identifying drugs fargeting the protein for treatment of disorders apoptosis related disorders and bacterial infection.
                                                                                                                                                                                                                                                                                                                                    TMFR1, tumour necrosis factor receptor, polymorphism; human;
tumour; cancer; apoptosis; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Algebrater ovar caracter and an action of the Hilling Hillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 100,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nandabalan K, Schulz VP, Stephens JC, Chew A;
                                                                                                                                                                                                                                                                Human tumour necrosis factor receptor 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seq 1/1 to. AAB23446 from. 1 to: 455
                                    AAB23446 standard, Frotein, 455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 5; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0121314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-2000; 2000WO-US04606
                                                                                                                                                                                    CD JAN 2001 (First entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 5.466
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEPHENS J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-543909/49.
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHULZ V P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200050436-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHEW/) CHEW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1999;
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                                                                                                                AAB23446;
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51 GCTGTTGSTGGGAAFAFAGGGGTFAFTGGACFGGFGGCFCAGC 100

- 17 uLeuLeuValdlyIleTyrProSerGlyValIleGlyLeuValProHisL 34
- 151 CACCCICAAAAIAAIICGAIIIGTIGIAGCAAGIGGGGACAAAAGAAAGIA 200 51 HisProGlnAsnAsnSerlleCysCysThrLysCysHisLysGlyThrTy 67
- 201 CTTGTACAATGACTGTCCAGGCCCGGGCAAAAAAAGGGACTGCAGGGAGT 250
- GTGAGAGGGGCTFCACCGCTTFCAGAAAACCACCTCAGACACTGCCTC 300
- 84 yecluserolyserPheThrAlaSerGluAsoHisCysLeu 199
- 301 AGTIGCTCCAAATGCCGAAAATGCCGTCAGCTCGGAGAIGTCTTCTTG 350
- 351 CACASTOSACCOSSANACOSTSTSTSSCIPTOTAGAAAGAACAACAACACTAGASCAGA 400 117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
- 401 AFTATTÖGAGTGAAAAAGTTTPGAGTGATTAAFTGGAGGGTGTGCTG 450
- 451 AATGGGALCGTWANTINTWINTWAGAGAAANWAAAWAAAWATGTGTGAN 500
- 501 Clearateradatiticiticitandadamaaamigagigicicargiaata 550
- 551 ACTGTAAGAAAGGGTGGAGTGCAAGATGTGCCTACGCCAGATTGAG 600
- 651 CALITICITIGGICHIGGCHIIAICCCICHCAIGGILIAAIGT 700
  - 217 lilePhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetT 234
- 70] APPORTAMENTAL TO GRANDE TO TATE TO TAKE TO THE TOTAL TO THE TAKE THE

- 801 GGCCCCAAACCCAAGCIICAGICCCAGICCAGGCIICACCCCCAACAAA 850
  - uAlaProAsnProSerPheSerProIhrProGlyPheThrProThrLeuG 284 797
- GCT.ICAG1CCCG1GCCGAG1.CCACTTCAACTTAACATTATAACTTATAACT 284 lyPheSerPinValPinSerSerThrPheThrSerSerThrThrThr 300
- 901 occusitida (Tistoto CAA) TTT so santono canada Sasetoso ACCACC 950 301 ProdlyAspCysPtoAsoPbcAlaAlaProArgArgSiuValAlaProPr 317
- 951 CIATCAGGGGGTGACCCATCTTGGGACACACCTGGCTGCGACACCAA 10<u>00</u>

Seq\_tame=\_/%1162\_j\_j\_j\_haa\_jenese\_j\_jere seq\_j\_AA£555\_5,a...AAB31336

seq\_documentation\_block: ID AAB01336 standard; Protein; 455 AA. (filst entry) 000C-4ES 50 AABU1336;

51.14. death reseptor, apoptusis, programmed (c) death; FAS) INF-R1; IRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus; плшар.

INF-R1 death receptor,

Homo sapiens 

W0200034335-A2.

15 - JUN - 2000.

44WH-US26035. 13-DEC-1999; 3801 0205018. 04 - DEC - 1 998,

(SCHE ) SCHERING CORP.

Leong C, Phillips JH;

MP1: 2009-424486,36.

Firified or remarkings, polypeptide for modifating apoptosis comprises a sequence which binds to an antibody specific for UL144 or its

risclosure, Hage 65 67, 75pp; English. FARETAX SX CCC

A pure or recombinant polypeptide which binds to a polypolonal antibody specific for the mature ULI44 is useful for screening molecules which

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block induction of apoptosis or interfere with antiapoptotic activity. The polypoptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or adevelopment, such as cancer or degenerative conditions and for requiation of viral infection and replication. At least five different death receptors are known, which include the CD95 (EASAPO-1), the TWY receptor 1, TWY receptor apoptosis-mediated protein (TMAMP), death receptor-6 (DR-6), and TWY-related apoptosis-inducing ligand (TPALL) receptors 1, 2 and 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 AA;
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Aliqn seq 1/1 to: AAB01336 from: 1 to: 455

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Gaps:

Quality: 2487.00

5.466

Ratio:

Percent Similarity: 106 886 alignment\_block: US-09-525-998A-1 x AAH01336

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1 ATGGGGCTCTCACTGTGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA
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51 GCIGITGGIGGGAAIAIACCCCTCAGGGGITATIGGAGIGGIGGCICACC 100 

101 TAGGGGACAGGGAGAGAGAGATAGTGTGTGTCCCCCAAGGAAAATATATC 150 4 PuGlyAspArgGluLysArqAspSerValCySProGloGlyLysTyrIle 151 CACCCTCAAAATAATTCGATTTGGTTGTACTAGTGGAAGGTA 200 51 HistrochinAssansortIcGysGysCystAistysCysHistysClyThrTy

201 CITGIACAATGACIGTCCAGGCCCGGGGCAGGATACGGACIGCAGGAAGT 250  251 GTGAGAGGGGCTCCTTCAGGGCTTCAGAAAACCACTGAGAGAGTGGGGTG 300  101 SerCysSerLysCysArglysGluMetGlyGlnValGlulleSerSerCy 117

301

450 401 ATTALFGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC

167 151 AsnGlythrValHistenSerCysGlnGluLysGlnAsnThrValCysTh 

CTGCCATGCAGGTTTCTTTCTAAGAGAAAAGGAGTGTGTCTCCTGTAGTA 550 

000 55) ACTICIAAGAAAAGTTIGGAGIGCACGAAGTIGIGGGIAGCCCAGATIGAG 

andystystysSertoralludysThrtysteudysteipradlatiedla 200 AATGITAAGGGGACTGAGGACTCAGGGACCACAGTGCTGTTGCCCCTGGT 650 109

110 951 CTATCAGGGGGGTGACCCCATCGCTTGCGACACCCTCGCCTGCGGACCCCA 1000 1151 AGATYORATYOGGCTGGAGAGAGAGAGAGAGAGAGGGGGGGGGGGGGGGAA 1200 1251 GCT44A4TF4TF4A4AC4C4T4TCC4C4ACAC4AACAF4CT4ATG44CTGCC 1300 000 850 434 euGluAspIleGluGluAlaLeuCysGlyProAlaAlaLeuProProAla 450 317 ofyrGlnGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProl 334 384 luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400 651 CATITICITIGGICTITIGCOTTITATCCCTCCTCTTCALTGGITTAATGT 700 201 AsnValtySGlyThrCluAspSerClyThrThrValteuteuProLeuVa 217 701 AFCGCTACCAACGCFGGAAGTCCAAGCTCTACFCCAFTGFTTGFGGGAAA 851 GCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGGTCCACCTATACC 1051 CIAGACACIGATGACCCCGCGACGCTGTACGCCGTGGTGGAAGAACGACGCC 1101 OCCUTACACTESANSAATTAGTACAGCCTAGGGTGAGGACGACCACG 1001 TOCOCCAROCCETTCAGAAGTGGGAGGACAGCCCCACAGAGCCACAGAGC 751 TCGACACCIGAAAAAAAAGGGGAAGTTGAAGGAACTACTACTAACCCC 901 CONTROLLOR OF THE CONTROL OF CONTROL OF THE CON 1351 CCCAGTCTTCTCAGA 1365

seq\_name: /SIDS2/qcgdata/geneseq/geneseqp/AA2001.DAT:AAB36697 Ą AAB36697 standard, Protein; 455 seq\_documentation\_block:

AAH.35697;

451 ProSerLeuLeuArg 455

15-MAE-2001 (first eatry)

Human tumour necrosis factor receptor TNFR1 protein SEQ 1D NO:3.

tunour necrosis faction related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective, antiviral; antiinflammatory; anticonvolsant; antiparasitie; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic reli death related disease; autoimmune disorder; cancer; cardiovascular disorder; viral intection. PRAIL receptor without intracellular domain; diagnosis; cytostatic; "s Joydeses Buman: tymour necrosis factor

Homo sapiens.

WO200071150-A1.

30-NOV-2000.

99US-0135164. 20-MAY-1999;

18-MAY-2000; 2000WO-US13515.

(HUMA-) HUMAN GENOME SCI INC 

Ni J;

Gentz RL,

Wei Y, Ruben SM,

WPI; 2001-041051/05.

Nucleic acid encoding a TRID polypeptide, also referred to as tumor neerosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection -

Disclosure; Fig 2; 285pp; English

The present invention describes the human TRID protein (tumour necrosis factor (TNF) related appropriate intradellular domain, also referred to as tumour necrosis factor receptor Without controls facellular domain, also referred to as tumour necrosis factor receptor 5 (TMTR-5 or TR5). TRID has extostatic, innumensuppressive, nontropic, neuroprotective, antivital, antiinflammatory, anticonvulsant, antiparasitic, and and the anti-face the antiparasitic, and and be used in gene therapy. The TRID polynucleotides are useful for detecting compenentary polynucleotides. TRID proteins and parasite, bacteria and viruses, restences and graft versus host disease. They are also useful for inducing proliteration of T-cells, endothelial cells and certain hermatoperial or repulse antivital responses and to prevent certain autoimmune diseases after stimulation of TRID by an about the TRID perpulse are useful for treating analyzer results and to prevent certain autoimmune diseases after stimulation of TRID by an about a TRID by an about a TRID by an about a treating analyzer preventing diseases and the prevent certain autoimmune diseases after stimulation of TRID by an about the treating analyzer preventing diseases. Associated with increased or decreased apoptotic cell death. The TRID polynorleadides, profesions, and includists and antaponists are useful to the diagnosis. Lreatment or prevention of. (a) cancer.

(b) autolmmune disorders; (c) diseases associated with increased apoptosis; (d) various associated with increased apoptosis; (d) various associated with increased apoptosis; (d) various associated to the increased apoptosis; and various associated with increased comparison with TRID in the exemplification of the present invention.

455 AA

alignment\_scores:

Percent Identity: 109.000 Length: Gaps: Percent Similarity: 195,888 Ouality: 2487 00 5.466 Ratio:

455

US-09-525-998A-1 x AAR36697 alignment\_block:

Align seg 1/1 to: AAB36697 irom: 1 to: 455

51 GCTGTTGGTGGGAAATAIACCTCAGGGGTIAIIGGACTGGTCCCTCACC 100 

1	AND	<b>.</b>
101 34	GGGACAGGGAGAAGAGAGAGAGAGAGGGGGGGGAAGAAAAAA	150 50
12.5	COSTGANALAATTOOALLIGGISTAGIAGIGGOOFAAASGAAGGAALLIGHAAAAAAAAAAAAAAAAAAAAAAAAAAAA	200
201	TGTACAATGACTGTCCAGCCCGGGGCAGGATGCGTTTTC TTTCTTTTTTTTTT	25u 84
251	AGCGGCTGGTTCACCGCTTCACAAAACCACCTGAGA TTFFTTTTTTTTTTTTTTTTTTTTTTTTTTT SerGTgSet PhethralaSerCtuasiH:stouatt	300
301	GCTOTAALGCCAAAAGAAATGGGTAGTG 	350
351	ACACCGGGGGGGGGGAGGAGAAAAA HIIIHHHHHHHHHHH SPIhYSAGIYCYSAFGLYSASGG	406 134
40i 134	i i doag i caaaaacci i i i Coag i och i chaa i i och och och och i i i i i i i i i i i i i i i i i i i	450 150
451	1966ACOTGOACOTHECHGOASSAGAAACAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	50.0
501	CATGERAGE ETTECTANGAAAA GAGEGGGGGGGGGTETTETTETTETTETTETTETTETTETTE	550 184
551	AGAAAAGCOOGAAGOAGAAGTIGIGGCOAGGCO 11   1   1   1   1   1   1   1   1   1	500 200
(1) (1) (2) (3)	FOITANSSERVITGASSACIPTASSERVITATATETTE STEELE OLIG HTTTTT TELEFORMER OLIGINALE TELEFORMER OLIGINALE STEELE	650 217
651	FFG H 63 CFF6000 FTATOORSTOH A FGSTEAM 	700
791	2007AC/AA/3010GAAG192AACG1/1AG12CA1931131333 	250
751	NO. 1-7AAAAAAGAGGGGGAGGTIAAAGAGAAATA 1711 	80%
801	DOGAAACOAGGOTTOAGOGGAO OGAGGOTTOAOOGGAOOTTOAOOGGAOOTTO OGAGAA OGAGAAA OGAGAAAAAAAAAA	9 5 8 5 5 4 8 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
851 284	AGTCOORTCCCAGTTCCACCTTCTCCTCCAGGTGCAGCTATA FILLITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	300
901 301	NOTTEGGGCLOCCGCGGASAGAAL 	950
951	CTATCAGGGGGGGTGCCTGGGACCCGTGGGACCCGA HTHTHTHTTTHTHTHTHTHTHTHTHTHTHTHTHTHTHT	3,44

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Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cycleine residue cross linked with polyethylene \eta_1 \gamma \phi \phi_1, useful for treating inflammatory and degenerative diseases mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF inhibitor; antiinflammatory; Tumour Necrosia Factor, interleukin.
IL-1: inflammatory disease; degenerative disease; human.
051 CHAGAMACTICATGAMMAMMAMMIGHAMMAMMINGHGGAGAAGGHGGC 1100
                                                                                                                                                1251 GCTGGAAGTGGTGGGACGCGTGCTCCGCGACATGGACTTGCTGGGCTGCC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 obrotouArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisC 384
                                                                                                                                                                                                                                                                                                                                                                                                                    417 rl.cuGluLeuLeuGlyArgValLcuArgAspMetAspLcuLeuGlyCysL 434
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                                                                                                                                                                      King MW, Bale KK, Brewe.
RW, Vannice J, Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 30 kDa TNF inhibitor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
10 AAB37677 standard, protein; 455 AA
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18-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-PER-1990;
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The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37678 and AAB37685), which have TNF inhibitors activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (LL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the precursor for 30 kba TNF inhibitor can inhibit TNF alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GCTGTTGGTGGGAATATAPPPPTTGAGGGGTTAITASAPPGSTGAGGGCTCACC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 TAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 CACCCICAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 TIGIAGANGATGATGGGAGGGGGGGGAGATAGGGAGTGGAGGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ATRACACIONITOTITORCONITCAGAAAANIANIINAGACIGOOLO 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 CACAGTGGACCGGGAACACCGTGTGTGGGTGCAGGAACAAAAAATAAGTAAAGGGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 ATTATTGGAGTGAAAAACTTTTCCAGTGCTTCAATTGCAGCCTGTGCCTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 AATGGGACCGTGCACCTCCTCCTCCAGGAGAACACACGCGTGTGCAC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 rCysHisAlaClyPhePheLeuArgCluAshCluCysValScrCysScrA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGGCCTTACCCCAGATIGAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGCTGCTCCAAATGCCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 FIGURAGASSITTTTTTAAGAAAAAAAGAGIGIGIGIGIGIGIAGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGGCCTCTPPAPPGTGAPPTGAPPTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 uLeuleuValGiylleTyrProSerGlyVallleGlyleuValPtoHisi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity, 100,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                 Example 6, Fig 21, 82pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAB37677
                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-525-998A-1 x AAB37677
                                                                                                                                                                                                                                                                                                                                               Quality: 2487 On
                                                                                                                                                                                                                                                                                                                                                                   5.466
                                                                                                                                                                                                                                                   455 AA;
                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                        Sequence
× 2 × 0 0 0 0 0 0 0 0 × 3
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601 AATGTTAAGGGGACTGAGGACTGAGGCACAGGGCTGTGTTGTTGCCGCCGGGT 650

us-09-525-998a-1.rag

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1051 CTAGACACTGATGACOCCGGGACOCTGTACGCCGTGGTGGAGAACGTGCC 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 CCCGIIGCGCIGGAAGGAAIICGIGCGCGCCIAGGGCIGAGCGACCACGCG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1201 TAMAMMATOTTSSCREPTISTAGSCSSCAGSSCSSCSSSSSSSAGSCAG 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AssivaligsOlgThrOlaAspscrClgThrThrValLeuLeuProLeuVa 217
                                                          651 CAITITCILIGGICILIGGGGILIFARGGGIGGIGGIGALTGGTTAATGT 790
                                                                             701 ATCCTACCAACGCTCCAACTCCAACCTCTACTCCATTGTTGTGCGAAA 750
                                                                                                                                                               751 TOGACACCTGAAAAAGAGGGGGGAGTTFGAAAGAAATAATTAATTAAGAGGGGTA 800
                                                                                                                                                                                                                                             267 uAlaProAsnProSerPheSerProThrProGlyPheThrProThilicuG 284
                                                                                                                                                                                                                                                                                                                                                                                     851 GCTTCAGTCCCCGGGTGCTTCCACCTTCACCTCCGAGCTCCACCTATACC 900
                                                                                                                                                                                                                                                                                                                                                                                                           284 lyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 OCCURATIONAL OFFINATION OF SOCIOES ASSESSED SOCIOES AS U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ProGlyAspCysProAsnPhcAlaAlaProArgArgGluValAlaProPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 rieuGluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysl, 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: //slisz/qopjajata_pepepeng-pepepengpyAA1991.DAT:AAK11082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 leproAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11082 standard, Protein, 455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 55kD TNF-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY 1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1351 CCCAGTCTTCTCAGA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 ProSerlieuLeuArg 455
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Partial amino acid sequences were determined for the 55 and 75kb in BBS (see ARE 1072 R1981) and oligometeride primers were synthesised based on these partial sequences. The primers were used to profeed a CNA transfel in the no apprice is after a biman placeful cDNA bank constructed in lambda will positive clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifed and sequenced. UNA constructs comprissed the INF bi coding sequence may also contain a fragment enroding a human 1g domain. Recombinant constructs are used to transform cells to conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding them, useful in pharmaceutical prods, and for antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                       imple Z, Sentz R. Lesslaudt W. Lotscher H:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insoluble tumour necrosis factor binding proteins - and DNA
                                                                                 Zlabel - putative N-qlycosylation site
                                                                                                                                         Alabel- putative N alycosylation site
                                                                                                                                                                      [abe] putative N giyeosymathom site
                                                                                                               /label= putative N-qlycosylation site
                          autoimmune alometalonephritis: lyaphokine, cyckine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 99.780
                                                                                                                                                                                                    /label- transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
            Tamout Nectosis Factor, binding profeits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aliqn seq 1/1 to: AAF11082 trom: 1 to: 455
                                                                                                                                                                                                                               /label- signal peptide
                                                       arration/gralitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improved INF-binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE AG.
                                                                                                                                                                                                                                                                                                                       99EP-0116767
                                                                                                                                                                                                                                                                                                                                                  · 'H-0001347.
                                                                                                                                                                                                                                                                                                                                                                 E9.7H-0003319.
                                                                                                                                                                                                                                                                                                                                                                               90CH-0000746.
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Ratio: 5.459
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US-09-525 998A l x AAR11082
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N-PSDB; AAQ10955.
                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 455 AA;
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                                                                     Modified site
                                                                                               Modified-site
                                                                                                                             Modified-site
                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Brockhaus M.
                                                                                                                                                                                                                                                                                                                      31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                   20 - APR-1990:
                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1990;
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                                                                                                                                                                                                                                                             EP417563-A.
                                                                                                                                                                                                                   Peptide
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51 GUIGIIGA PAGAATATA DOCICAGGA HATIGGACIGGICO JUACACO 100 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17

1 AIGGGCTTTTTATTGIOTCTGACTIOTTGCIGGGACTGTTTTGGA 50

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201 CITGIACAAIGACIGTGTGTAGGGGGGGGGGAGAGAGAGAGGGAGGGGGGGT 250
                                                                                                                                                                                                                                        251 GTGAGAGGGGCTTCTTCACGGTTTCAGAAAACCACCTCAGAGACIGCCTC 300
                                                                                                                                                                                                                                                             301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTG 350
                                                                                                                                                                                                                                                                                                                                             351 CACAGIGGACTGGGATACTGTGGGTTGTGGTAGAAGAACCAGTACCGGGC 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                          117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 CIGCCAIGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCTGTAGTA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIGINAAGAAAAGOPYGGAATIGINAPGAATITGIIGEETTAGGGEOAGATITGAG KOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 rCysHisAlaGlyPhePheLeuArgGluAshGluCysValSerCysSerA 184
                                        34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle 50
                                                                                                       67 rl.euTyrAshAspCysProGlyProGlyGlnAspThrAspCysArgGluC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 ATTATTGCAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AshVallysClyThrCluAspScrClyThrThrValLeuLeuProLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 CATTITCTITGGTCTITGCCTTTTATCCTCCTCTTCATTGGTTTAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 ATEGETACEAAGGGTGGAAGTGGAAGCTGTACTCCATTGTTGTGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 GGCCCCAAACCCAAGCTTCAGTCCCAAGCTTCAGCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 uAlaProAsnProSerPheSerProThrProOlyPheIhrProThrLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           851 GGTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 CCCGGTGACHGTCCCAACTTTGCGGCTCCCCGGAGAGGTGGCACCACC
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Tumour necrosis factor alpha; autoimmune diseases; cachectin;
||001||TCCCCAACCCCCTTCAGAAGTGGGAGGAGAGGCCCAGAAGGCAGAGAGC ||050
                                            1051 CTAGACACTGACCCCCCCAGACGCTGTACACCGTGACGAAGAACGTGAC
                                                                                                                                                                              1201 TACAGCATGCTGGCGACCTGGAGGTGGTGCAGGCCGCGAGGGGGGCCAC 1250
                                                                                                                                                                                                                         367 oProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG 384
                                                                                                                                                                                                                                               417 rLeuGluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL 434
                                                                                                                                                                                                                                                                                                                                                             Seq_name /SIDS2/4~4data/yeneseqp/AA1992.DAT:AAR20787
          101 CCGTTGCGTGGAA34AATTCGTGTGGGGCTGAGGGGACCAC
                                                                                                                                  1151 AGATTGATTGGGTTGTATTGTAGAAGGGGGGGTGGTGCCCGGGGGGGCGAA
                                                                                                                                                                                          "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "potential N-glycosylation site"
                                                                                                                                                                                                                                     7moc.
7mote: "extrace]lular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brennan F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..455
ote- "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               AAR20787 standard, Protein; 455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray P, Turner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90GB-0013410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF-alpha binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .153
                                                                                                                                                                                                                                                                                                                1351 CCCAGTCITCICAGA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145..147
                                                                                                                                                                                                                                                                                                                                      451 ProsertieuLeuArg 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extracellular domain.
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                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block
                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAR20787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
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The amino acid sequence is that of tumour necrosis factor alpha binding protein which contains the extracellular domain of human TNF alpha receptor. It is soluble and can be used in the regulation of TNF-mediated responses by binding and sequestering the cytokine. It can therefore be used the repeatically to treat disorders such as carboxia, sepsis and autolimnunc discases, specifically rheumatoid
                                                                              New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 CIIGIACAAIGACIGICTAGATCIGGGGGGATAGGAIACGATIGTAGGGAGI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 GIGAGAGGGGTICALCOCTICAGAAAACCACTITAGACACIGCCTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCIGCICCANATGCCGANAGGANATGGGICAGGIGGAGAICICITG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 CACACTGGACTGGGACACTGTGTGTGGTTGCAGGAAGAACTAGTACGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01 IAGGGGACAGGGAGAGAGAGATAGIGTGTGTCCCCAAGGAAATATATC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 CACCCTCAAAATAATTCGAATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 HishroCinAsnAsnScriteCysCysCystbilgSysHistysClyIbrTy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AIGGGCCICICCACCITACTICACTICATOTACTACTACTACTAGA 50
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Percent Similarity: 100 000 Porcent Identity: 94 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 455
                                                                                                                                                                 Disclosure: Fig 1: 25pp; English.
                                                                                                                            e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seq 1,1 +0: AAP20787
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 2481.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-525-998A-1 x AAR20787
                     WPI: 1992-043613/06.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 455 AA.
                                         N-PSDB; AAQ20973
                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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951 CTATCAGGGGGTTGACCCCATCCTFGCGACAGGCFTGGCGTGCGGACCCCA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 AGALCGATCGGCLGGAGTIGCAGAACGGGCGCLGGCLGGCGGGGAGGGGAA 1200
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                                                                                    BUL AAIGIIAAGGGAANIGAGGANIGAGGAATAAGIGTIGIIGOOLIGGI 650
                                                                                                                                                                                                           701 ATCCCTACCAACGGGGAAGICCAAGGICIACIGGAIIGIIIGIGGGAAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                  851 GCTICAGISSISSISSISSISSAGITICSAGETTEASSISSISSAGISSAGIATAGE 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 lulleAspArglouGlubeuGlnAsnGiyAraCysteuArgS.sAlaGln 4u0
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                                                        551 ACIGIAAGAAAAGCCIGGAGTGCACGAAGIIGIGAA AGCCCAGAIIGAG 640
                                                                                                                                                                                                                                                                                               651 CAITITGILEST CITTGGCHITTATGGGTGFICHGHGAGHGH 700
                                                                                                                                                                                                                                                                                                                                                        217 lilePhePheGlyLeuGysLeuLeuSerLeuLeuPheIleGlyLeuMetJ 234
167 rCysHisAladlyPhePheLeuArddluAsmilluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 LOGACACOLGAMMAAAAGGGGGGCTTCAAGGAACTACTAACTAAGCCCCT
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SOU\_hafter, [31 42] p. plata, principly reself, AA1931...A..AAA42197

seq\_dorumentation\_block:

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deletion modulates signal transduction and/or elecadage effected by the receptor. This modulation of activity can also be achieved using effected by the receptor. This modulation of activity can also be achieved using effects proteins which interact with the TNE receptor or the elector proteins which interact with the TNE receptor or the elector proteins can be used to treat or prevent discuses associated with the activity e.g. autoimmune discuse; rhoundool arthritis; graft to TNE activity e.g. autoimmune discuse; rhoundool arthritis; graft to be used to treat overdoses of example of specific deletions. Include amino acid sessions of them which it was discovered that amino acids 405-414, or part of them, are essential for the signalling of the human p55 TNP-R for the expensive effect of TNP whereas amino acids 415-426 are not essential. Also residues 170-179 whereas amino acids 415-426 are not essential. This region of amino acids, or part of, when deleted, abolished shedding of the amino acids, or part of the protein.
                                                                                                                                                               rheumatoid arthritis; graif rejection; graft vs. host; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modification of the tumour necrosis factor receptor by mutation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medalating activity of tumbur measurs factor receptor rusing peptide(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto-immune
                                                                                                                                              INF; tumour necrosis factor; receptor; disease; autoimmunity;
                                                                                                                                                                                                                                                                                                                                 /label- Transmembrane domain.
                                                                                                                                                                                                                                                                                          /label- Leader peptide
                                                                                                         p55 Tumour necrosis factor receptor
                                                                                                                                                                                                                                                          Location/Qualifiers
AAR42197 standard; Protein; 455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Figure 1; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           93EP-0106981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, septic shock, etc.
                                                                         (first entry)
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                                                                                                                                                                                effector protein.
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                                                                       13-MAY-1994
                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1993
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                                                                                                                                                                                                                                                                           Region
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Personnt Identify. 90 560 Gaps: Quality: 2478.09 Ratio: 5.446 Ratio: 5.446 Percent Similarity: 100.000aliqnment\_scores:

Align seg 1/1 to: AAR42197 from: 1 to: 455 alignment\_block: US-09-525-998A-1 x AAR42197

1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCCACTGGTGCTCCTGGA 50

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301 AGCTGCTCCAAATGCCGAAAGGAAATGGCTCGGCGGGAGATCTCTTG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 ALCOCTACTARACTOGAGICCAAGCICTACTGGATTGTTTGTGGAAA 750
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                                                                                                                                                                                                                           INT TRAGGGACAGGGAGAGAGAGATAGTGTGTGTGTGCGCAAGGAAAATATATG
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501 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA
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rheumatoid arthritis: graff rojoofion; graff vs. host; septic shock,
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                                                 951 CTATCAGGGGGTGACCCATCTTGCGACAGCCCTCGCCTCGGACCCCA 1000
                                                                                                                                                   .001 PCCCCAACCCCCIICAGAAGIGGAAGACAGGGCCACAAAGCAAAAGA 1050
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                                                                                               317 ofyrdisdlyalaAsphrolleLedalaThralaLedAlaScrAsphrol 334
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                                                                                                                                                                                                                                                                                    /label- Transmembrane domain
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/label- Leader peptíde.
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A Modification of the fumbur necrosis factor receptor by mutation or deletion modulates signal transduction and/or clearage effected by the receptor. This modulation of activity can also be achieved using effector. This modulation of activity can also be achieved using effector proteins which interact with the TWF receptor or the effector. Molecules with interact with the TWF receptor or the effector of proteins can be used to theat of prevent diseases associated with the activity e.g. autoimmute disease or septic shows They can also be acted to treat the disease or septic shows They can also include amino acids residues 405.42 from which it was discovered that amino acids 465.44, or part of them, are essential for the signalling of the human p55 TWFR for the cytotoxic effect of TWF whereas amino acids 465.44, or part of them, are essential for the whenevers amino acids 415.45 are not cascuttal. Also residues 170-174, 174-179 or part of the acids 450-179 were deleted. This region of amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soluble extracellular forms of the protein. This sequence solution and the wild type protein discussed in AAM-4219 except that alanine at postion 197 has been substituted in place of serinc. The substitution inhibits cleavage of the soluble form of the
                                                                              Modulating activity of tamour accrosis factor receptor using peptide(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GCIGIIGGIGGGAAIAIACCCICAGGIIAIIGGAGGGICCTCACC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TAGGGGACAGGAGGAAGAGATAGTGTGTGTGTTTAAGGGAAAATATATC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 CACCCTCAAALAALLCGATITGCTGTACCAAGLACGAAAAAAAACCTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 CHRIADANISACIGIC AGCOCGGGGCAAANACGGACTGCAGGAGI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GIGAGGGGGTGCTTCARCATTGACAAACCACTCACAGAGGCTGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 AGRIGGICCAAATGOCGAAAGGAAATGGGTCAGGTGGAGATGTCTTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MctGlyLcaSerThrValProAspleateaLeaLeaFroFcaValLeaLeaGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 euglyAspArad_uLysArgAspSerValCysFroGlnGlyLysTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 rheufyrAshAspCysProGlyProGlyGinAsplhrAspCysArgGinC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGGCC FC FGCACCGTGCTGACTTGCTGCTGCCACTGGTGCTCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 99.441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 455
                                                                                                                                                                                                                Claim 5: Figure 1: 17pp; English.
                                                                                                                                                                aisease, septir shock, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.440
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAR51034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-525-998A-1 v AAP51034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 2475.00
1993 17:017,45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 455 AA;
                         N-PSDB; AAU50870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
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351 CACAGIGGAN GUGACACIGIGIGACIGOAGAAGAANAALAAGGGC 466

- 401 ATTATIGGAGIGAAAACCTITITCCAGIGCTICAATTGCAGCCICIGCCTC 450
  - 134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
- 451 AATGGGACCGTGCACCTCCTGCCAGGAGAACAGAACACCGTGTGCAC 500
- 501 CTGCCATGCAGGTTTCTTTTCTAAGAAAAGAGTGTTGTCCTTGTAGTA 550
- 551 ACTGTAAGAAAAGCCTGGACTGCACGAAGTTGTGCCTACCCCAGATTGAG 600
- - AATGTTAAGGGCATTGAGGACTFCAGGCACCACAGTGTTGTTGCCCCTGGT-650 601
- 651 CATTITICLITIGGICTITIGGCTTTTATGCCTCCTCCTTCATTGGTTTAATGT 700 217 HHEPHER PROGREGUE OF A FRANCE OF THE HER PROGREGUE TO THE PROPRIET THE PROGREGUE OF THE PROGREGUE TO THE PROGREGUE OF THE
- 701 ATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTGTGGGGAAA 750
- 751 TCGACACCTGAAAAAGAGGGGGGGGCTTCAAGGAACTACTAAGCCCCCT 800
- 801 GORGERAAGERAAGERTAGAGEREAGEREAGGEREAGGERGGAGG 850
  - 267 uAlaProAsnProSerPheSerProThrProGlyPheThrProThrLeuG 284
- 851 GCTTCAGTCCCGTGCCCAGIICCACCIICACCICCAGCICCACCIATACC 900
- 901 COCCOLCANTOTONAAPTITACOTOTOTOTOTACAGAGGGGGGCACCACC 950
- 951 CIAICAGGGGCIGAGCCCAIGGTTGGGAGAGGCGIGGGCIGCGAGGCCA 1000
- 1001 TCCCCAACCCCTTCAGAAGTGGGGAATAGGGGCCACAAGGCACAAGACTAGGC T050 334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350
- 1051 CIAGAMATICAIGAMMONOMONIGHAMONOMIGIGGNGGAGAAGGNGGG 1100
- 1101 CCCCTTGCCCIGGAAGGAATFCCTGCGGCCCTAGGCCTGAGCGACCACG 1150 351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr 367

367 oProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG 384

- |201 | TACAGRATIONTINGPRANTINGAGINGPRANTINGAGING | 1250
  - 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417

1251 GCTGGAGCTGGTTGGGAGGCGTGCGGGGAGATGGAGCTGCTGGGCTGCC 1300

- 417 rheuGluicufeuGlyArgValbeuArgAspMetAspLeufeuGlyGyst 434

- 1351 CCCAGFCTTCTCAGA 1365
  - 451 ProSerLeuLeuArg 455

